

097D61 ID 097D61 PRELIMINARY; PRT; 217 AA.
 AC 097D61;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Amino acid ABC transporter, permease component.
 GN CAC3619.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Brelton J., Omeichenko M.V., Makarova K.S., Zeng Q.,
 Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
 Tatusov R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
 Bennett G.N., Koonin E.V., Smith D.R.;
 "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum."
 J. Bacteriol. 183:4823-4838(2001).
 RL EMBL; AB007858; AAK81542.1;
 DR InterPro; IPR000515; BPD_cranep.
 DR Pfam; PF00528; BPD_cranep.1.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBERS.1.
 KW Complete proteome.
 SQ SEQUENCE 217 AA; 23743 MW; 36738BCDCDE9A2F CRC64;

Query Match 9.2%; Score 88.5; DB 16; Length 217;
 Best Local Similarity 24.8%; Pred. No. 0.25;
 Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLHAICPCQLRCSSTPPTTCORVCNAY-----TNSYKGTNAI---LMTCLGI 62
 DB 4 SSLNKYIPVLDTRITTLTLCSSIIIGCITGITIAMFKTSSVKVNLGKPYTWLRGT 63
 QY 63 SLTSLAVFY--LMTFLRKISSEPLRDEF-----KNTGS-----GLGMANIDKSR 108
 DB 64 PLHLQLYVYVYGLPFLSDKLTMTMPMAAIIIGLSLNSGAYIAETIRGIIAIDNGQPEASK 123
 QY 109 -----TGDDEIILPRGLEVTVEEC-----TCEDCI-KSKPKVSDH 142
 DB 124 ALGLTYGGMKRIITLFOAIRVVPICGNERIAMIKDTSLVSVTMELLRKQLLVSSSG 163
 QY 143 CFFLPAMEGA--TIVTTKTNDYCSLPAALSATEIKSIS 182
 DB 184 DAVTPYLPAGIFVYLITLTITFTGIFSK-----IEKKLS 215

RESULT 3
 ID 08R056 PRELIMINARY; PRT; 842 AA.
 AC 08R056;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 94.5 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028286; AAH28286.1; -.
 KW Hypothetical protein
 SQ SEQUENCE 842 AA; 94478 MW; 734C10D715E5BC92 CRC64;

Query Match 9.0%; Score 86.5; DB 11; Length 842;

Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPCOLRCSSTPPTTCORVCNAYSTNSVKNALMTCLGLSLIISLAVFLMEL 77
 DB 126 LVGCFCCRC-----CNK-CGSEMHOROKONAPRRRCGLSLIVGLMSLGI 176
 QY 78 RKISEPPLKDEPKNTGSLGMANIDKSRGTD-EIIL---PRGLEVTVECTCE---- 129
 DB 177 GVVAAQQRTRIKRGOK-----LAKSNFRDQTLTETPKQIDIVVQYNTXKA 227
 QY 130 ---DCIKS-----KPKVSDHCFPLPAMEGATILVTK-TNDYCSLPAAL- 172
 DB 228 FSDLIGISVLCGRIKDQKPKV-----TPVLEIRKAMATAIKOTDALQNMSSSLKS 280
 QY 173 ---SATEIKSISA 183
 DB 281 LQDAATQALNTNLS 294

RESULT 4
 ID 09Y1X8 PRELIMINARY; PRT; 1193 AA.
 AC 09Y1X8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Protein tyrosine kinase.
 GN EPTK178.
 OS Ephydatia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haplosclerida; Spongiaillidae; Ephydatia.
 OX NCBI_TaxID=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9246375; PubMed=10229568;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 Miyata T.;
 "Extensive gene duplication in the early evolution of animals before
 the parazoan-eumetazoan split demonstrated by G proteins and protein
 tyrosine kinases from sponge and hydra."
 J. Mol. Evol. 48:646-653(1999).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21601119; PubMed=11738833;
 RA Suga H., Katoh K., Miyata T.;
 "Sponge homologs of vertebrate protein tyrosine kinases and frequent
 domain shufflings in the early evolution of animals before the
 RT parazoan-eumetazoan split."
 RL Gene 280:195-201(2001).
 DR EMBL; AB006570; BAA81724.2; -.
 DR HSSP; P08631; 1AD5.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR002290; Ser_thr_Pkinase.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR Prodom; PD000001; Euk_Pkinase; 2.
 DR SMART; SM00261; FU; 6.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 KW Kinase.
 SQ SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;

Query Match 8.9%; Score 85.5; DB 5; Length 1193;
 Best Local Similarity 22.3%; Pred. No. 3.6;
 Matches 37; Conservative 28; Mismatches 56; Indels 45; Gaps 8;

QY 2 LOMAGCCQNYFDSLALACIPQRCGSSNTP-----LTCQRYCNASTVNSVKTNAIL 56
 DB 715 LCVSGCSNDTEYQDAALN-CLPCAGCIGCGSPSISQCLTCA--SGSCITTDVOSGGII 771
 QY 57 WTCLGLSLIISLA---VFVLMFLRKISSEPLKDEFKYTGSLGMANIDLEKSRGDEI 113
 DB 772 GIVESIVIVPLATVIVILFVRYRREHKVFKNTQSTGTA--MCKYSN-----GNET 820
 QY 114 ILPRGLETVVECTCEDCIKSKPVSDH---CPLPAMEGART 155
 DB 821 LRP-----PKLPDARTLRIITPRTALBGGQVL 847

RESULT 5

Q8RWV7 PRELIMINARY; PRT; 938 AA.

Q8RWV7 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 103.6 kDa protein.
 GN ATG48195.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida Y., Jones T.,
 RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinzaki K.,
 RA Davis R.W., Becker J.R., Theologis A.,
 RT "Arabidopsis Full Length cDNA Clones."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091078; AAM13898.1;
 KW Hypothetical protein.
 SQ SEQUENCE 938 AA; 103602 MM; 3E78395D65D75C95 CRC64;

Query Match 8.7%; Score 83.5; DB 10; Length 938;
 Best Local Similarity 29.4%; Pred. No. 4.5;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

QY 38 QRYCNASTVNSVKTNAILMTCLGLSLIISLAVFLMLRKISSEPLKD-EFKN--TGS 94
 DB 29 ERYCSA---NSALGTSPW---C-----SSTGPRQDSFEFNFSYGP 62
 QY 95 GLGMANIDLEKSRGDEIILPRGLETVVECTCEDCIKSKP-----KVSDHCEPLPAM 149
 DB 63 SLVLTSSIDM--SRIGD-----RGTHFDEGSCNGRSSAPGLNTGNTVNDMCGDL--M 113
 QY 150 EEGATI 155
 DB 114 DGGATI 119

RESULT 6

Q9STR8 PRELIMINARY; PRT; 1998 AA.

Q9STR8 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 13, Last annotation update)
 DE Hypothetical 223.5 kDa protein.
 SQ T24C20_80.

OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choisme N., Robert C., Brottier P., Wincker P., Catolico L.,
 RA Ariguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Quetier P., Salanoubat M.,
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL096856; CAB51067.1;
 DR InterPro; IPR000515; BPD_transp.
 DR InterPro; IPR001683; PX.
 DR Pfam; PF00787; PX; 1.
 DR SMART; SMO0312; PX; 1.
 DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1998 AA; 223513 MM; 8B3D6A03CD248F55 CRC64;

Query Match 8.7%; Score 83.5; DB 10; Length 1998;
 Best Local Similarity 29.4%; Pred. No. 11;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

QY 38 QRYCNASTVNSVKTNAILMTCLGLSLIISLAVFLMLRKISSEPLKD-EFKN--TGS 94
 DB 1089 ERYCSA---NSALGTSPW---C-----SSTGPRQDSFEFNFSYGP 1122
 QY 95 GLGMANIDLEKSRGDEIILPRGLETVVECTCEDCIKSKP-----KVSDHCEPLPAM 149
 DB 1123 SLVLTSSIDM--SRIGD-----RGTHFDEGSCNGRSSAPGLNTGNTVNDMCGDL--M 1173
 QY 150 EEGATI 155
 DB 1174 DGGATI 1179

RESULT 7

Q97491 PRELIMINARY; PRT; 327 AA.

Q97491 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Fas protein.
 GN FAS.
 OS Ovis aries (sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takagi M., Takahashi H., Kabeya H., Ohaishi K., Sugimoto C., Onuma M.,
 RT "Cloning of sheep fas antigen."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB011671; BAA37093.1;
 DR HSPB; P25445; IDDP.
 DR InterPro; IPR00488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR SMART; SMO0005; DEATH; 1.
 DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00117; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 SQ SEQUENCE 327 AA; 36928 MM; 5CFEB844B2BE387A CRC64;

[illegible]

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RESULT 8
08VEV6
ID Q8VEV6 PRELIMINARY; PRT; 314 AA.
AC Q8VEV6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Olfactory receptor MOR202-36.
OS Mus musculus (Mouse).
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse. ";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY073792; BAL6455.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1.1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2.1.
RECEIPT:
SEQUENCE. 314 AA; 34996 MW; 9C7B11A5917EA632 CRC64;

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Oy      8 CSQNEPFLSLHACP-CQLRCSNNT-----PLTLQRRCMAVSYNSVGTAAIIMT 58
Db      146 CYMCIQDIQSSIVVALAFCLSFCSNVYINHFCDIDPL-IDIGSDIYINEL--TVIILGT 202

Query Match 8.5%; Score 81.5; DB 11; Length 314;
Best Local Similarity 30.4%; Pred. No. 2.1;
Matches 31; Conservative 16; Mismatches 40; Indels 15; Gaps 6

Oy      59 CLG-LSLIISLAVFLMP--LTKIISSEPLKDEPKNTGSGLL 97
Db      203 CDGIITLLVLIINTVLLIFPAIRKMSAEQKRAFTSCAHLI 244

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RESULT 9		
094711		
ID	PRELIMINARY;	PRT; 223 AA.
AC	094711	
DT	01-FEB-1997 (TREMblrel_02, Created)	
DT	01-FEB-1997 (TREMblrel_02, Last sequence update)	
DT	01-DEC-2001 (TREMblrel_19, Last annotation update)	
DE	51C surface protein.	
	Parametium tetraurella.	

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;
OC Paramoecium
OX NCBI_taxid=5886;
RN
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=92106337; PubMed=1762150;
RA Nielsen B., You Y., Forney J.;
RT "Cysteine residue periodicity is a conserved structural feature of
RT variable surface proteins from *Paramoecium tetraurelia*."; J
RL J. Mol. Biol. 222:835-841(1991).
DR EMBL; M65164; AAA61740.1; --
DR Interpro; IPR002895; Paramoecium_SA.
DR Pfam; PF01508; Paramoecium_SA; 25.
SQ SEQUENCE 2233 AA; 237078 MW; C064FE0AF7B8873B CRC64;

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Query Match      8.5%; Score 81.5; DB 5; Length 2233;
Best Local Similarity 25.1%; Pred. No. 20;
Matches 43; Conservative 17; Mismatches 58; Indels 53; Gaps 10

QY      6 GGCQNEYPEDSLHACIPQCRCSNTPPLTCORYCNA-SVTSVKGTAIIMTCLGLSL 64
Db      520 GSCYQKQ-----CSAASQDNTHAQCEYLPACTLSNWKKG-----CIDPL 561

QY      65 IISLAVLIMFLRKISSEPLKDEPKXTGSSLLGMANIDL-----EKSRIGDEIILPRGLE 120
Db      562 TCSA-----LIVENGECLKANREK---CMTGSTCVDPICTTAPTKTDD-----D 603

QY      121 YVVEEECT---EDCIRKSKPKVDSDHCFPLPAMEGATI-----LVTTKTN 162
Db      604 YVVELEAVKPSNCV---PNGTKKGCMEELAAKESRTILEQCDVAGTKTN 651

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ID	Q39191	PRELIMINARY;	PRT;	595 AA.
AC	Q39191;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Serine threonine kinase.			
GN	PRO25.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eumariophyta; Vitridiplanetae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsis.			
CC	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	MEDLINE=3306369; PubMed=1436303;			
RA	Smith T.A., Kohorn B.D.;			
RT	"An Arabidopsis serine threonine kinase homologous with an EGF repeat			
RT	selected in yeast for its specificity for a thylakoid membrane			
RT	protein."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL; L04999; AAA3844.1; -			
DR	InterPro; IPR000152; Aex_hydroxyl.			
DR	InterPro; IPR000561; EGF-like.			
DR	InterPro; IPR001861; EGF_Ca.			
DR	InterPro; IPR000719; Euk_pkinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	Pfam; PF00069; pkinase; 1.			
DR	ProDom; PD000001; Euk_pkinase; 1.			
DR	SMART; SM00179; EGF_Ca; 1.			
DR	SMART; SM00001; EGF_like; 1.			
DR	PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.			
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.			
DR	PROSITE; PS01187; EGF_Ca; 1.			
DR	PROSITE; PSS0001; PROTEIN KINASE DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST_1.			
DR	ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; kinase;			
DR	Repeat; Serine/threonine-protein kinase; transferase.			

SQ SEQUENCE 595 AA; 65899 MW; 7858FC1A6560641 CRC64;
 Query Match 8.4%; Score 81; DB 10; Length 595;
 Best Local Similarity 24.5%; Pred. No. 4.9;
 Matches 39; Conservative 27; Mismatches 49; Indels 44; Gaps 10;

QY 8 CSONEYFDSLHACIPQ--LRCSN-----TPPLTCOR-----YCN-----SV 45
 DB 127 CRCEGFGDNPYLSAGCQDVNCTTSSTIRHNCSDPTCKRKVGFGYCKCGGYRLDPT 186
 QY 46 TNSVK-----GTNAIWTCLGLSLISLAVFVLMFLRKISSEPLKDE-FKRTSGGL-- 97
 DB 187 TMSCKRKEFAWTTILVTTTIGF-LVILLGVACIQQRMKHLKDTLRLEQFPEONGGMLTQ 245
 QY 98 ---GMANID-----LEKRTG--DEIILPRGLETV 123
 DB 246 RLSGPSNDVAKITFEDGKMKATNGVAESRIILGCGGQGTIV 284

TLT 11
 92
 AC 001892 PRELIMINARY; PRT; 773 AA.
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RO8F11.7 protein.
 GN RO8F11.7
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE=99069613; PubMed=9851916;
 RX None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.",
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Mink P.;
 RT "The sequence of C. elegans cosmid RO8F11."
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF003385; AAB54249.1; --
 DR HSSP; P05164; ICP.
 DR InterPro; IPR002007; Anim_peroxidase.
 DR Pfam; PF03098; An_peroxidase; 1.
 SQ SEQUENCE 773 AA; 83992 MW; 4E3373FDA4EC67C7 CRC64;

Query Match 8.4%; Score 81; DB 5; Length 773;
 Best Local Similarity 21.7%; Pred. No. 6.6;
 Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;

QY 23 PCOLRCSNTPLTCQ-----RYCN-----ASTNSVKGNTALMTCL--GSL 64
 DB 184 PPKSNATQGGFPKSSDPSVHRIRISITGYCNNRGKPTQANSVTARLRILGTTSTYDGLQ 243
 QY 65 IISLAVFLMFLRKISSEPLKDEPKNTG-SGLGMANIDLEKSGTGEIILPRGLETV 123
 DB 244 IRNYSVTSPPLSTLISNKLHDEGSTNFPSPVHLMQIGQFIADIIIFPSSAKDG 303
 QY 124 EECCEGDIKSKPKYDSDHCFPLPAMEGATILVTTTKNDYCKSLPALSA-----TE 176
 DB 304 SSLNCTSC--SSPTTISTNCAPIPAPADKRYFTVPSRTAECIRLTRALNQGSGFVRTQ 361

QY 177 IEKS 180
 DB 362 IDON 365

RESULT 12
 ID 081820 PRELIMINARY; PRT; 735 AA.
 AC 081820;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Wall-associated kinase 1 (putative wall-associated kinase 1).
 GN WAK1 OR F16F4.6
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99308512; PubMed=10380805;
 RA He Z.H., Cheeseman I., He D., Kohorn B.D.;
 RT "A cluster of five cell wall associated receptor kinase genes, wak1-5,
 RT are expressed in specific organs of Arabidopsis.",
 RL Plant Mol. Biol. 39:1189-1196(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
 RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Tracy S.E.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F16F4.6 (GI:8920634).";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ009696; CA08794.1; --
 DR EMBL; AY039917; AA64021.1; --
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF CA.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR004040; STY_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00179; EGF CA; 1.
 DR SMART; SM00001; Euk_pkinase; 1.
 DR SMART; SM00221; STYC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Kinase;
 KW Repeat; Serine/threonine-protein kinase; transferase.
 KM Repeat; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 735 AA; 81211 MW; AAD41A28296093B6 CRC64;

Query Match 8.3%; Score 80; DB 10; Length 735;
 Best Local Similarity 24.2%; Pred. No. 8;
 Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps 10;

QY 8 CSONEYFDSLHACIPQ--LRCSN-----TPPLTCOR-----YCN-----SV 45
 DB 264 CRCEGFGDNPYLSAGCQDVNCTTSSTIRHNCSDPTCKRKVGFGYCKCGGYRLDPT 323
 QY 46 TNSVK-----GTNAIWTCLGLSLISLAVFVLMFLRKISSEPLKDE-FKRTSGGL-- 97
 DB 324 TMSCKRKEFAWTTILVTTTIGF-LVILLGVACIQQRMKHLKDTLRLEQFPEONGGMLTQ 382

```
Oy      98 -----GMANID-----LEKSRGTG--DEIILPRGLETVV 123
          |::|         ::|       :   |::|
Db      383 RLSGAGPSNVDKIFTEDEGMKKATNGYAESRILGGGGQGV 423
```

RESULT 13

ID	026489;	PRELIMINARY;	PRT;	1299	AA.
AC	026489;				
DT	01-NOV-1996	(TREMblrel. 01, Created)			
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)			
DT	01-JUN-2002	(TREMblrel. 21, Last annotation update)			
DE	Endoprotease	furin.			
GN	FURIN.				
OS	Phylum: Chordata				
OS	Subphylum: Vertebrata				
OS	Class: Mammalia				
OS	Order: Carnivora				
OS	Family: Canidae				
OS	Genus: Canis				
OS	Species: Canis lupus				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia				
OC	Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.				
NCBI	_taxid=7108;				

Query Match	8.2%	Score	79.5	DB	5	Length	1289
Best Local Similarity	24.1%	Pred. No.	1.7				
Matches	39	Conservative	26	Mismatches	48	Indels	49
						Gaps	11

```

0Y      8 CSONEYFOSLIHACIPCOLRCS-----SNTPLPTGORCNMS-----VTNYSVGTNAIL-W 57
      1150 CSRPLRIRLRANNOQAPC-----CSERGVNSTPPTDC-CHCNPNNGECJNSSVAGKRRIAEW 1205
0Y      58 TGLGIS-----LTIISLAV-----FVLMFLRLKRSSEPLKDFEFGNTSGLLGMAN 101
      1206 GALTTPASADAPSVAVVTIAACAAGLFTVLVALVLAHSSREKRTRKTSVRG----- 1255
Db
0Y      102 IDLEKSRGTDEIILPR-GLEYTVEECTCEDCIKSPKYDSH 142
      1260 --VEYSR-----LPTDVDPFV-----LTSCTDQCGPVEYEH 1289

```

RESULT	14
OSVFWO	
ID	OSVFWO
AC	OSVFWO
DT	01-MAR-2002 (TREMBLrel. 20. Created)
DT	01-MAR-2002 (TREMBLrel. 20. Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21. Last annotation update)
DE	Olfactory receptor MOR202-16.
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).

Query Match	8.1%;	Score 78.5;	DB 11;	Length 314;
Best Local Similarity	30.4%;	Pred. No. 4.4;		
Matches 31; Conservative	15;	Mismatches	41;	Indels 15; Gaps 6;

```

QY  CSQNEXFEDSLHACIP-COLRCSNPT-----PPLCQRKYCNASVYKNGNALMT 58
Db  146 CYNCGGLQSSIHVALAFCLSPNSVNVNHFCDIPPL-LDSCSDYITNEI--TVLLIGT 202
QY  59 CLG-LSLIISLAVFLMF--LIRKISSEPLKDFKNTGSGLL 97
Db  203 CGGILTLVLVNTYLLIFPAIRNMSVSAOKRAFTCSAHLI 244

```

RESULT	15		
Q9H677			
ID	Q9H677	PRELIMINARY;	PRT; 485 AA.
AC	Q9H677;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	CDNA: FLJ22531.f01, clone HRC12890.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kaasabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okita R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,		
RA	Tanaka T., Nakamura Y., Isegaki T., Sugano S.,		
RT	"NEDD human cDNA sequencing project."		
RL	Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.		
RL	EMBL: AK02184; EMBL5387.1; -		
SO	SEQUENCE 485 AA; 54051 MW; 4474B549ACD560C3 CRC64;		

Query Match.	8.1%;	Score	78.5;	DB	4;	Length	485;
Best Local Similarity	26.3%;	Pred. No.	7.2;				
Matches	35;	Conservative	17;	Mismatches	48;	Indels	33;
				Gaps			6.

```

Qy 47 NAKGNNALIMTLCIGSLISLAVELVFLARKISSEELKDFKNQTS-----GLGM 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 NRISVSIFLYGRLGFLPILS-----TWEGQMTTFPFKDTSSLVDWKYKXHCMI 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 100 ANIDLEKSRGTGDEIILPRGLETVTECTCEDCISKPK-----VDSHCPLEPAME 150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 233 PRIDLMLDR---DLVLP-DVSIVQVSESESDSQMDPQGOTLLFLFVDFHSAFVQOME 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 151 -EGATILVTTKTN 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 IMGVYTLITLTHLN 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: June 23, 2003, 08:39:06
Job time : 85.0818 secs